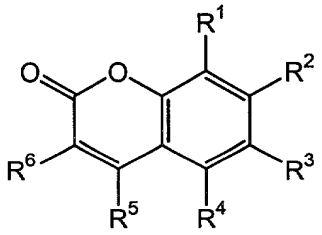
WHAT IS CLAIMED IS:

1. A material having a fluorogenic moiety linked to a solid support, said material having the structure:



wherein:

R^1, R^2, R^3, R^4, R^5 and R^6 are members independently selected from the group consisting of H, halogen, $-NO_2$, -CN, $-C(O)_mR^7$, $-C(O)NR^8R^9$, $-S(O)_tR^{10}$, $-SO_2NR^{11}R^{12}$, $-OR^{13}$, substituted or unsubstituted alkyl, $-R^{14}$-*SS*, and $-NHR^{15}$ with the proviso that at least one of R^1, R^2, R^3, R^4, R^5 and R^6 is $-R^{14}$-*SS* and at least one of R^1, R^2, R^3, R^4, R^5 and R^6 is $-NHR^{15}$,

wherein:

R^7, R^8, R^9, R^{10}, R^{11}, R^{12} and R^{13} are members independently selected from the group consisting of H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl;

R^{14} is a linking group adjoining said fluorogenic moiety and said solid support;

R^{15} is a member selected from the group consisting of amine protecting groups, -C(O)-AA and -C(O)-P:

wherein:

P is a peptide sequence;

AA is an amino acid residue;

m is a member selected from the group consisting of the integers 1 and 2;

t is a member selected from the group consisting of the integers from 0 to 2; and

SS is a solid support.

2. The material according to claim **1**, wherein said linking group is a member selected from the group consisting of substituted or unsubstituted alkyl, substituted or unsubstituted heteroalkyl and substituted or unsubstituted aryl;

3. The material according to claim **1**, wherein P is a peptide sequence comprising the structure:

$$-C(O)-AA^1-AA^2-(AA^i)_{J-2}$$

wherein,

AA^1-AA^2-$(AA^i)_{J-2}$ is a peptide sequence, wherein each of AA^1 through AA^i is an amino acid residue which is a member independently selected from the group of natural amino acid residues, unnatural amino acid residues and modified amino acid residues;

J denotes the number of amino acid residues forming said peptide sequence and is a member selected from the group consisting of the numbers from 2 to 10, such that *J*-2 is the number of amino acid residues in the peptide sequence exclusive of AA^1-AA^2; and

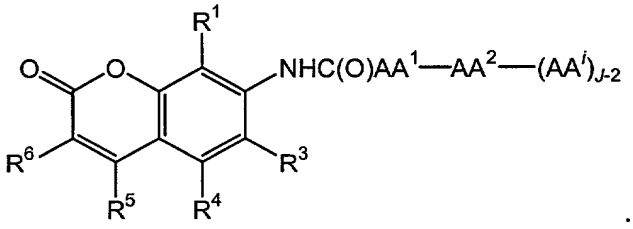
i denotes the position of said amino acid residue relevant to AA^1 and when *J* is greater than 2, *i* is a member selected from the group consisting of the numbers from 3 to 10.

4. The material according to claim **1**, wherein R^{15} has the structure:

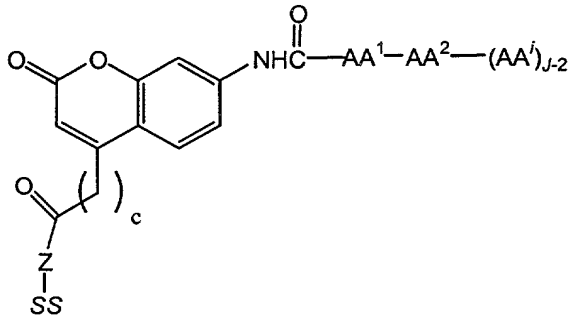
$$-C(O)-AA;$$ and

AA is an amino acid residue selected from the group consisting of natural amino acids, unnatural amino acids and modified amino acids.

5. The material according to claim **1**, having the structure:



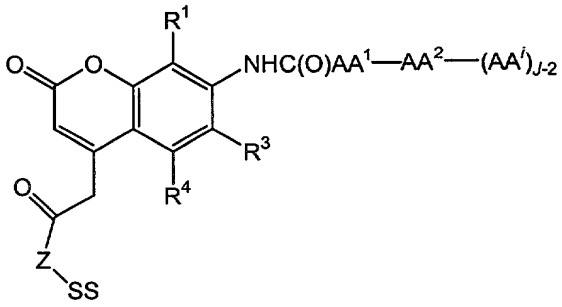
6. The material according to claim **5**, having the structure:



wherein, Z is a member selected from the group consisting of –O-, and –-NR^{16}-; and

c is a member selected from the integers from 0 to 6.

7. A material according to claim **6**, having the structure:



8. A method of assaying for the presence of an enzymatically active protease in a sample, said method comprising:

(a) contacting said sample with a material according to claim **3** in such a manner whereby said fluorogenic moiety is released from said peptide sequence upon action of said protease, thereby producing a fluorescent moiety; and

(b) observing whether said sample undergoes a detectable change in fluorescence, said detectable change being an indication of the presence of said enzymatically active protease in said sample.

9. The method according to claim **8**, wherein said protease is a member selected from the group consisting of aspartic protease, cysteine protease, metalloprotease and serine protease.

10. The method according to claim **8**, wherein said protease is a protease of a microorganism.

11. The method according to claim **10**, wherein said microorganism is a member selected from the group consisting of bacteria, fungi, yeast, viruses, and protozoa.

12. The method according to claim **8**, wherein said sample is a clinical sample from a subject.

13. The method according to claim **8**, further comprising (c) quantifying said fluorescent moiety, thereby quantifying said protease.

14. A method of assaying for the presence of a selected microorganism in a sample by probing the sequence specificity of peptide cleavage by a protease of said microorganism, said method comprising:

(a) contacting a sample suspected of containing said selected microorganism with a material according to claim **3**, wherein said peptide comprises a sequence that is selectively cleaved by said protease of said selected microorganism, thereby releasing the fluorogenic moiety from the peptide sequence;

(b) detecting the cleavage by detecting fluorescence arising from a fluorescent moiety produced by cleavage of said fluorogenic moiety from said peptide sequence, thereby confirming said presence of said selected microorganism in said sample.

15. The method according to claim **14**, further comprising (c) quantifying said fluorescence, thereby quantifying said protease of said microorganism.

16. A fluorogenic peptide comprising a fluorogenic moiety covalently bound to a peptide sequence, said peptide having the structure:

$$R\text{-}P$$

wherein:

P is a peptide sequence having the structure:

$$-C(O)\text{-}AA^{1}\text{-}AA^{2}\text{-}(AA^{i})_{J-2}$$

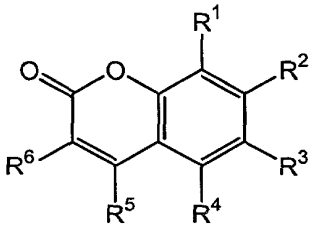
wherein:

each of AA^1 through AA^i is an amino acid residue which is a member independently selected from the group of natural amino acid residues, unnatural amino acid residues and modified amino acid residues;

J denotes the number of amino acid residues forming said peptide sequence and is a member selected from the group consisting of the numbers from 2 to 10, such that *J*-2 is the number of amino acid residues in the peptide sequence exclusive of AA^1-AA^2;

i denotes the position of said amino acid residue in sequence relative to AA^1 and when *J* is greater than 2, *i* is a member selected from the group consisting of the numbers from 3 to 10; and

R is a fluorogenic moiety having the structure:



wherein:

R^1, R^2, R^3, R^4, R^5 and R^6 are members independently selected from the group consisting of H, halogen, $-NO_2$, -CN, $-C(O)_mR^6$,$-C(O)NR^7R^8$, $-S(O)_tR^9$, $-SO_2NR^{10}R^{11}$, $-OR^{12}$, substituted or unsubstituted alkyl, -NHC(O)-P, and $-R^{20}$-Y, with the proviso that at least one of R^1, R^2, R^3, R^4, R^5 and R^6 is $-R^{20}$-Y and at least one of R^1, R^2, R^3, R^4, R^5 and R^6 is -NHC(O)-P,

wherein:

R^6, R^7, R^8, R^9, R^{10}, R^{11} and R^{12} are members independently selected from the group consisting of H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl;

R^{20} is either present or absent and is a member selected from the group consisting of substituted or unsubstituted alkyl and substituted or unsubstituted heteroalkyl;

Y is a member selected from the group consisting of organic functional groups and methyl;

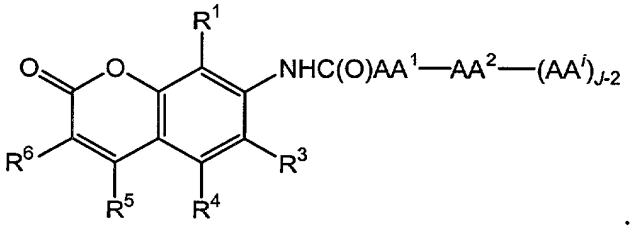
m is a member selected from the group consisting of the integers 1 and 2; and

t is a member selected from the group consisting of the integers from 0 to 2.

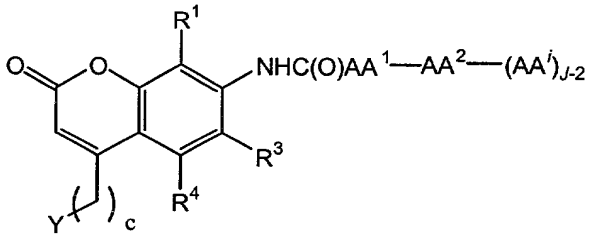
17. The fluorogenic peptide according to claim **16**, wherein said organic functional group is a member selected from the group consisting of $-COOR^{17}$, $CONR^{17}R^{21}$, $-C(O)R^{17}R^{21}$, $-OR^{17}$, $-SR^{17}$, $-C(O)SR^{17}$ and $-NR^{17}R^{21}$

wherein, R^{17} and R^{21} are members independently selected from H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl.

18. A fluorogenic peptide according to claim **16**, having the structure:



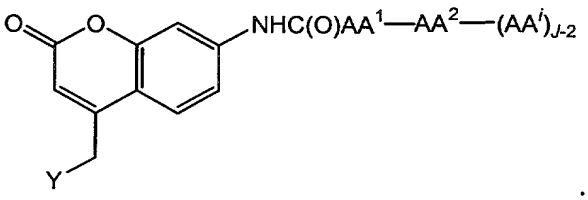
19. A fluorogenic peptide according to claim **18**, having the structure:



wherein:

c is a member selected from the group consisting of the integers from 0 to 6.

20. A fluorogenic peptide according to claim **19**, having the structure:



21. The fluorogenic peptide according to claim **16**, wherein said peptide sequence comprises a peptide bond that is cleaved by a protease releasing said fluorogenic moiety from said peptide sequence, thereby producing a fluorescent moiety and a peptide moiety.

22. The fluorogenic peptide according to claim **21**, wherein said peptide bond is formed between a carboxyl of the carboxy-terminus amino acid residue and an amine group of said fluorogenic moiety.

23. A method of assaying for the presence of an enzymatically active protease in a sample, said method comprising:

(a) contacting a sample suspected of containing said protease with a peptide according to claim **16** in such a manner whereby said fluorogenic moiety is released from said peptide sequence upon action of said protease, thereby producing a fluorescent moiety; and

(b) observing whether said sample undergoes a detectable change in fluorescence, said detectable change being an indication of the presence of said enzymatically active protease in said sample.

24. The method according to claim **23**, wherein said protease is a member selected from the group consisting of aspartic protease, cysteine protease, metalloprotease and serine protease.

25. The method according to claim **23**, wherein said protease is a protease of a microorganism.

26. The method according to claim **25**, wherein said microorganism is a member selected from the group consisting of bacteria, fungi, yeast, viruses, and protozoa.

27. The method according to claim **23**, wherein said sample is a clinical sample from a subject.

28. The method according to claim **27**, wherein said subject is a human.

29. The method according to claim **23**, further comprising (c) quantifying said fluorescent moiety, thereby quantifying said protease.

30. A method of assaying for the presence of a selected microorganism in a sample by probing the sequence specificity of peptide cleavage by a protease of said microorganism, said method comprising:

(a) contacting a sample suspected of containing said selected microorganism with a material according to claim **16**, wherein said peptide comprises a sequence that is selectively cleaved by a protease of a selected microorganism, thereby releasing said fluorogenic moiety from said peptide sequence;

(b) detecting said cleavage by detecting fluorescence arising from a fluorescent moiety produced by cleavage of said fluorogenic moiety from said peptide sequence, thereby confirming said presence of said selected microorganism in said sample.

31. The method according to claim **30**, further comprising (c) quantifying said fluorescence, thereby quantifying said protease of said microorganism.

32. A library of fluorogenic peptides comprising at least a first peptide having a first peptide sequence covalently attached to a first fluorogenic moiety and a second peptide having a second peptide sequence covalently attached to a second fluorogenic moiety, said first peptide and said second peptide having the structure:

R-P

wherein:

for each of said first peptide and said second peptide, P is independently selected from peptide sequences having the structure:

$$-C(O)-AA^1-AA^2-(AA^i)_{J-2}$$

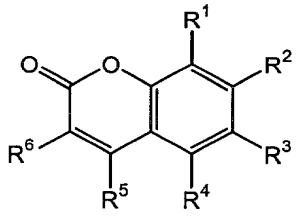
wherein:

each of AA^1 through AA^i is an amino acid residue which is a member independently selected from the group consisting of natural amino acid residues, unnatural amino acid residues and modified amino acid residues;

each J is independently selected and denotes the number of amino acid residues forming said first peptide sequence and said second peptide sequence and is a member selected from the group consisting of the numbers from 2 to 10;

each i is independently selected and denotes the position of said amino acid residue relative to AA^1 and when J is greater than 2, i is a member selected from the group consisting of the numbers from 3 to 10; and

for each of said first peptide and said second peptide R is independently selected from fluorogenic moieties having the structure:



wherein:

R^1, R^2, R^3, R^4, R^5, and R^6 are members independently selected from the group consisting of H, halogen, $-NO_2$, -CN, $-C(O)_mR^7$, $-C(O)NR^8R^9$, $-S(O)_tR^{10}$, $-SO_2NR^{11}R^{12}$, $-OR^{13}$, substituted or unsubstituted alkyl, -NH-C(O)-P, R^{20}-Y and $-R^{14}$-*SS*, with the proviso that for each peptide at least one of R^1, R^2, R^3, R^4 and R^5 is a member independently selected from $-R^{14}$-*SS* and R^{20}-Y and at least one of R^1, R^2, R^3, R^4, R^5, and R^6 is -NH-C(O)-P,

wherein:

R^7, R^8, R^9, R^{10}, R^{11}, R^{12} and R^{13} are members independently selected from the group consisting of H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl;

R^{14} is a linking group adjoining said fluorogenic moiety and the solid support;

R^{20} is either present or absent and is a member selected from the group consisting of substituted or unsubstituted alkyl and substituted or unsubstituted heteroalkyl;

Y is a member selected from the group consisting of organic functional groups and methyl;

m is a member selected from the group consisting of the integers from 1 to 2;

t is a member selected from the group consisting of the integers from 0 to 2;

Y is a member selected from the group consisting of –$COOR^{17}$, $CONHR^{17}$, $-C(O)R^{17}$, $-OR^{17}$, $-SR^{17}$, and NHR^{17};

R^{17} is a member selected from the group consisting of H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl; and

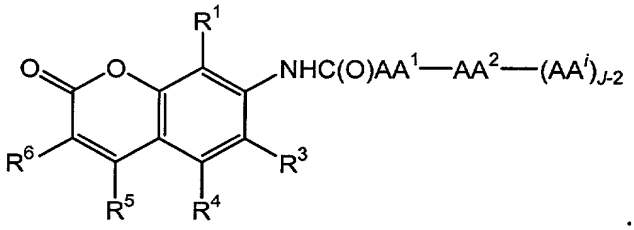
SS is a solid support.

33. The library according to claim **32**, wherein said linking group is a member selected from the group consisting of substituted or unsubstituted alkyl and substituted or unsubstituted heteroalkyl

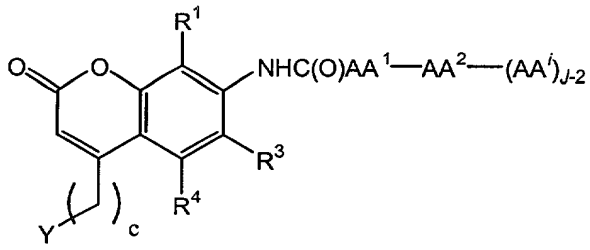
34. The library according to claim **32**, wherein said organic functional group is a member selected from the group consisting of –$COOR^{17}$, $CONR^{17}R^{21}$, $-C(O)R^{17}R^{21}$, $-OR^{17}$, $-SR^{17}$, $-C(O)SR^{17}$, and $-NR^{17}R^{21}$

wherein, R^{17} and R^{21} are members independently selected from H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl.

35. The library of fluorogenic peptides according to claim **32**, wherein R-P has the structure:



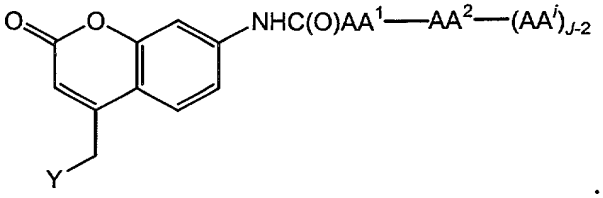
36. A library of fluorogenic peptides according to claim **35**, wherein R-P has the structure:



wherein,

c is a member selected from the group consisting of the numbers from 0 to 6.

37. A library of fluorogenic peptides according to claim **36**, wherein R-P has the structure:



38. The library according to claim **32**, wherein said fluorogenic moiety of said first peptide and said fluorogenic moiety of said second peptide are different fluorogenic moieties.

39. The library according to claim **32**, wherein said first peptide sequence and said second peptide sequence are identical.

40. The library according to claim **32**, wherein said first peptide sequence and said second peptide sequence are different.

41. The library according to claim **40**, wherein an amino acid residue selected from the group consisting of AA^1, AA^2, AA^i and combinations thereof of said first peptide is a different amino acid residue than an amino acid residue at a corresponding position relative to AA^1 of said second peptide.

42. The library according to claim **32**, wherein AA^1 of said first peptide sequence and AA^1 of said second peptide sequence are identical amino acid residues.

43. The library according to claim **32**, wherein AA^1 of said first peptide sequence and AA^1 of said second peptide sequence are different amino acid residues.

44. The library according to claim **32**, wherein AA^2 of said first peptide sequence and AA^2 of said second peptide sequence are identical amino acid residues.

45. The library according to claim **32**, wherein AA^2 of said first peptide sequence and AA^2 of said second peptide sequence are different amino acid residues.

46. The library according to claim **32**, wherein AA^i of said first peptide sequence and AA^i of said second peptide sequence are identical amino acid residues.

47. The library according to claim **32**, wherein AA^i of said first peptide sequence and AA^i of said second peptide sequence are different amino acid residues.

48. The library according to claim **42**, comprising at least six peptides having different peptide sequences, wherein AA^1 is a different amino acid residue in each of said different peptide sequences.

49. The library according to claim **48**, comprising at least twelve peptides having different peptide sequences wherein AA^1 is a different amino acid residue in each of said different peptide sequences.

50. The library according to claim **49**, comprising at least twenty peptides having different peptide sequences wherein AA^1 is a different amino acid residue in each of said different peptide sequences.

51. The library according to claim **32**, wherein AA^1 is a member selected from the group consisting of Lys, Arg, Leu and combinations thereof.

52. The library according to claim **32**, wherein J is a member selected from the numbers from 4 to 8.

53. The library of peptides according to claim **32**, wherein at least one of said first peptide and said second peptide is cleavable by a protease into a fluorescent moiety and the peptide sequence.

54. The library according to claim **32**, comprising at least 10 peptides, wherein each of the peptide sequences is a different peptide sequence.

55. The library according to claim **54**, comprising at least 100 peptides, wherein each of the peptide sequences is a different peptide sequence.

56. The library according to claim **55**, comprising at least 1,000 peptides, wherein each of the peptide sequences is a different peptide sequence.

57. The library according to claim **56**, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence.

58. The library according to claim **57**, comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence.

59. The library according to claim **58** comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence.

60. The library according to claim **32**, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate.

61. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising:

(a) contacting said protease with a library of peptides according to claim **32** in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;

(b) detecting said fluorescent moiety;

(c) determining the sequence of said peptide sequence, thereby determining said peptide sequence specificity profile of said protease.

62. The method according to claim **61**, further comprising (d) quantifying said fluorescent moiety, thereby quantifying said protease.

63. A database comprising at least one set of peptide sequence specificity data for a protease determined using a library according to claim **32**.

64. The database according to claim **63**, wherein said database is an electronic database.

65. The database according to claim **64**, wherein said database is distributed on a wide area network.

66. A database comprising at least one set of peptide sequence specificity data for a protease determined using a method according to claim **61**.

67. The database according to claim **63**, wherein said database is an electronic database.

68. The database according to claim **64**, wherein said database is distributed on a wide area network.

69. The method according to claim **61**, wherein said protease is a member selected from the group consisting of aspartic protease, cysteine protease, and serine protease

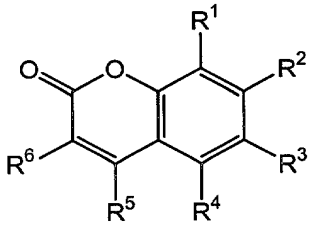
70. The method according to claim **61**, wherein said protease is a protease of a microorganism.

71. The method according to claim **70**, wherein said microorganism is a member selected from the group consisting of bacteria, fungi, yeast, viruses, and protozoa.

72. The method according to claim **61**, further comprising (c) quantifying the fluorescent moiety, thereby quantifying said protease.

73. A method of preparing a fluorogenic peptide, said method comprising:

(a) providing a first conjugate comprising a fluorogenic moiety covalently bonded to a solid support, said conjugate having the structure:



wherein,

R^1, R^2, R^3, R^4, R^5 and R^6 are members independently selected from the group consisting of H, halogen, $-NO_2$, -CN, $-C(O)_mR^7$,$-C(O)NR^8R^9$, $-S(O)_tR^{10}$, $-SO_2NR^{11}R^{12}$, $-OR^{13}$ $-NR^{18}R^{19}$, and substituted or unsubstituted alkyl, with the proviso that at least one of R^1, R^2, R^3, R^4, R^5 and R^6 is $-NH_2$;

R^7, R^8, R^9, R^{10}, R^{11}, R^{12}, R^{13}, R^{18} and R^{19} are members independently selected from the group consisting of H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl;

m is a member selected from the group consisting of the numbers from 1 to 2;

t is a member selected from the group consisting of the numbers from 0 to 2;

R^5 and R^6 are members independently selected from the group consisting of H and $-R^{14}$-C(O)NH-*SS*, wherein at least one of R^5 and R^6 is $-R^{14}$-C(O)NH-*SS*;

R^{14} is a member selected from the group consisting of substituted or unsubstituted alkyl and substituted or unsubstituted heteroalkyl;

SS is a solid support;

(b) contacting said first conjugate with a first protected amino acid moiety (pAA^1) and an activating agent, thereby forming a peptide bond between a carboxyl group of pAA^1 and the aniline nitrogen of said first conjugate;

(c) deprotecting said pAA^1, thereby forming a second conjugate having a reactive AA^1 amine moiety;

(d) contacting said second conjugate with a second protected amino acid (pAA^2) and an activating agent, thereby forming a peptide bond between a carboxyl group of pAA2 and said reactive AA^1 amine moiety; and

(e) deprotecting said pAA^2, thereby forming a third conjugate having a reactive AA^2 amine moiety.

74. The method according to claim **73**, further comprising:

(f) contacting said third conjugate with a third protected amino acid (pAA^3) and an activating agent, thereby forming a peptide bond between a carboxyl group of pAA^3 and said reactive AA^2 amine moiety; and

(e) deprotecting said pAA^3, thereby forming a fourth conjugate having a reactive AA^3 amine moiety.

75. The method according to claim **73**, further comprising between steps (b) and (c) capping aniline amine groups that have not reacted with pAA^1.

76. The method according to claim **75**, wherein said capping utilizes a mixture comprising an active ester of a carboxylic acid.

77. The method according to claim **78**, wherein said active ester is the nitrotriazole ester of acetic acid.

78. The method according to claim **74**, wherein a member selected from the group consisting of pAA^1, pAA^2, pAA^3 and combinations thereof comprises a mixture of protected amino acids differing in the identity of the amino acid portion of the protected amino acids.

79. The method according to claim **78**, wherein said mixture comprises at least 2 unique amino acids.

80. The method according to claim **79**, wherein said mixture comprises at least 6 unique amino acids.

81. The method according to claim **80**, wherein said mixture comprises at least 12 unique amino acids.

82. The method according to claim **81**, wherein said mixture comprises at least 20 unique amino acids.

83. The method according to claim **78**, wherein said mixture is an isokinetic mixture.